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☐ 1: Q96PY6. Serine/threonine-...[gi:22256934]

BLink, Domains, Links

LOCUS Q96PY6 1258 aa linear PRI 15-SEP-2003
 DEFINITION Serine/threonine-protein kinase Nek1 (Nima-related protein kinase 1) (NY-REN-55 antigen).
 ACCESSION Q96PY6
 VERSION Q96PY6 GI:22256934
 DBSOURCE swissprot: locus NEK1_HUMAN, accession Q96PY6;
 class: standard.
 extra accessions: Q9Y594, created: Feb 28, 2003.
 sequence updated: Feb 28, 2003.
 annotation updated: Sep 15, 2003.
 xrefs: gi: [15620860](#), gi: [15620861](#), gi: [5360120](#), gi: [5360121](#)
 xrefs (non-sequence databases): GenewHGNC:7744, MIM [604588](#),
 InterProIPR000719, InterProIPR008271, InterProIPR002290,
 InterProIPR001245, PfamPF00069, PRINTSPR00109, ProDomPD000001,
 SMARTSM00220, PROSITEPS00107, PROSITEPS50011, PROSITEPS00108
 KEYWORDS Transferase; Serine/threonine-protein kinase; ATP-binding; Mitosis;
 Nuclear protein; Phosphorylation; Cell cycle; Cell division;
 Tyrosine-protein kinase; Alternative splicing.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 1258)
 AUTHORS Nagase,T., Kikuno,R. and Ohara,O.
 TITLE Prediction of the coding sequences of unidentified human genes.
 XXI. The complete sequences of 60 new cDNA clones from brain which
 code for large proteins
 JOURNAL DNA Res. 8 (4), 179-187 (2001)
 MEDLINE [21456161](#)
 PUBMED [11572484](#)
 REMARK SEQUENCE FROM N.A. (ISOFORM 1).
 TISSUE=Brain
 REFERENCE 2 (residues 1 to 1258)
 AUTHORS Scanlan,M.J., Gordan,J.D., Williamson,B., Stockert,E., Bander,N.H.,
 Jongeneel,C.V., Gure,A.O., Jager,D., Jager,E., Knuth,A., Chen,Y.-T.
 and Old,L.J.
 TITLE Antigens recognized by autologous antibody in patients with
 renal-cell carcinoma
 JOURNAL Int. J. Cancer 83 (4), 456-464 (1999)
 MEDLINE [99438124](#)
 PUBMED [10508479](#)
 REMARK SEQUENCE OF 444-1258 FROM N.A. (ISOFORM 2).
 TISSUE=Renal cell carcinoma
 COMMENT -----
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 collaboration between the Swiss Institute of Bioinformatics and
 the EMBL outstation - the European Bioinformatics Institute.

The original entry is available from <http://www.expasy.ch/sprot>
and <http://www.ebi.ac.uk/sprot>

[FUNCTION] PHOSPHORYLATES SERINES AND THREONINES, BUT ALSO APPEARS TO POSSESS TYROSINE KINASE ACTIVITY. IMPLICATED IN THE CONTROL OF MEIOSIS (By similarity).

[CATALYTIC ACTIVITY] ATP + a protein = ADP + a phosphoprotein.

[SUBCELLULAR LOCATION] Nuclear (Probable).

[ALTERNATIVE PRODUCTS] Event=Alternative splicing; Named isoforms=2; Name=1; IsoId=Q96PY6-1; Sequence=Displayed; Name=2; IsoId=Q96PY6-2; Sequence=VSP_004870; Note=No experimental confirmation available.

[SIMILARITY] Belongs to the Ser/Thr family of protein kinases. NIMA subfamily.

FEATURES	Location/Qualifiers
<u>source</u>	1..1258 /organism="Homo sapiens" /db_xref="taxon:9606"
<u>gene</u>	1..1258 /gene="NEK1" /note="synonym: KIAA1901"
<u>Protein</u>	1..1258 /gene="NEK1" /product="Serine/threonine-protein kinase Nek1" /EC_number="2.7.1.37"
<u>Region</u>	4..258 /gene="NEK1" /region_name="Domain" /note="PROTEIN KINASE."
<u>Site</u>	10..18 /gene="NEK1" /site_type="np-binding" /note="ATP (BY SIMILARITY)."
<u>Site</u>	33 /gene="NEK1" /site_type="binding" /note="ATP (BY SIMILARITY)."
<u>Site</u>	128 /gene="NEK1" /site_type="active" /note="BY SIMILARITY."
<u>Site</u>	162 /gene="NEK1" /site_type="phosphorylation" /note="(AUTO-) (BY SIMILARITY)."
<u>Region</u>	478..521 /gene="NEK1" /region_name="Splicing variant" /note="Missing (in isoform 2). /FTId=VSP_004870."
<u>Region</u>	1232 /gene="NEK1" /region_name="Conflict" /note="G -> E (IN REF. 2)."

ORIGIN

```

1 mekyvrlqki gegsfqkail vkstedgrqy vikeinismr sskereesrr evavlanmkh
61 pnivqyresf eengslyivm dyceggdlfk rinaqkgvlf qedqildwfv qiclalkvhv
121 drkilhrdik sqnifltkdg tvqlgdfgia rvlntsvla rtcigtppy1 speicenpky
181 nnksdiwalg cvlyelctlk hafeagsmkn lvlkiisgsf ppvslhysyd lrslvsq1fk
241 rnprdrpsvn silekgfiak riekflspql iaefclktf skfgsqpipa krpasgqnsi
301 svmpaqkitk paakygipla ykkygdcklh ekkplqkhkq ahqtpekrvn tgeerrkise

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361 eaarkrrlef iekekqkdq iislmkaeqm krqekerler inrareggwr nvlsggsge
421 vkapflgsgg tiapssfsr gqyehyaif dmqqqraed neakwkrey grglpergil
481 pgvrpgfpyg aaghhfpa ddirktlkr kavskqanan rkgqlaver akqveeflqr
541 kreamqnkar aeghmvyar lrqirlqfn erqqikaklr gekkeanhse ggegseeadm
601 rrkieslka hanaraavlk eqlerkrkea yerekkwee hlvakgvkss dvspplgghe
661 tggspskqgm rsvsvtsal kevgvdsslt dtretseemq ktnnaisskr eilrrlnenl
721 kaqedekgkq nlsdtfeinv hedakeheke ksvssdrkkw eaggqlvipl deltdtsfs
781 tterhtvgev iklgpnspr rawksptds vlkilgeael qlqtellent tirseispeg
841 ekykplitge kkvcishei npsaivdspv etkspesfa spqmslkleg nleepddlet
901 eilqpsgtn kdeslpctit dvwiseeket ketqsadrit iqenevsedg vsstvdqlsd
961 ihiepgtnds qhskcdvdk vqpepfhkv vhsehlvlv qvqsvqcspe esfafrshsh
1021 lppknknkns lliglstglf dannpkmlrt csldpdklf rtmldvptvg dvrqdnleid
1081 eiedenikeg psdsedivfe etdtdlqelq asmeqllreg pgeeyseee svlknsvdvp
1141 tangtdvade ddpssesal neewhsdnd geiasececd svfnhleelr lhleqemgfe
1201 kffevyekik aihededeni eicskivqni lgnehghlya kilhlvmadg ayqednde

//

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Oct 14 2003 07:44:50

Comparison between SEQ ID NO:4 and Q96PY6

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAAUTa4Xs: 1214 aa

>seqid4

vs /tmp/fastaDAAVTa4Xs library

searching /tmp/fastaDAAVTa4Xs library

1258 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 40, opt: 28, gap-pen: -12/ -2, width: 16
Scan time: 0.034

The best scores are:

sp|Q96PY6|NEK1_HUMAN Serine/threonine-protein kin (1258) 4775

>>sp|Q96PY6|NEK1_HUMAN Serine/threonine-protein kinase N (1258 aa)
initn: 4773 init1: 4773 opt: 4775

Smith-Waterman score: 7822; 96.343% identity in 1258 aa overlap (1-1214:1-1258)

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seqid4	MEKYVRLQKIGEGSFGKAILVKSTEDGRQYVIKEINISRMSSKEREESRREVAVLANMKH					
	10	20	30	40	50	60
sp Q96	MEKYVRLQKIGEGSFGKAILVKSTEDGRQYVIKEINISRMSSKEREESRREVAVLANMKH					
	70	80	90	100	110	120
seqid4	PNIVQYRESFEENGSLYIVMDYCEGGDLFKRINAQKGVLFQEDQILDWVQICLALKHVV					
	70	80	90	100	110	120
sp Q96	PNIVQYRESFEENGSLYIVMDYCEGGDLFKRINAQKGVLFQEDQILDWVQICLALKHVV					
	130	140	150	160	170	180
seqid4	DRKILHRDIKSNIFLTKDGTVQLGDFGIARVLNSTVELARTCIGTPPYLSPEICENKPY					
	130	140	150	160	170	180
sp Q96	DRKILHRDIKSNIFLTKDGTVQLGDFGIARVLNSTVELARTCIGTPPYLSPEICENKPY					
	190	200	210	220	230	240
seqid4	NNKSDIWALGCVLYELCTLKHAFEAGSMKNLVLKIISGSFPPVSLHYSYDLRSLVSQFLK					
	190	200	210	220	230	240
sp Q96	NNKSDIWALGCVLYELCTLKHAFEAGSMKNLVLKIISGSFPPVSLHYSYDLRSLVSQFLK					
	250	260	270	280	290	300
seqid4	RNPRDRPSVNSILEKGFIKRIEFLSPQLIAEEFCLKTFSKFGSQPIPAKRPASGQNSI					
	250	260	270	280	290	300
sp Q96	RNPRDRPSVNSILEKGFIKRIEFLSPQLIAEEFCLKTFSKFGSQPIPAKRPASGQNSI					
	310	320	330	340	350	360
seqid4	SVMPAQKITKPAAKYGIPLAYKKYGDKKLHEKKPLQKHQAHQTPEKRVNTGEERRKISE					

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sp|Q96 SVMPAQKITKPAKYGIPLAYKKYGDKLHEKKPLQKHQAHTPEKRVTNGEERRKISE
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      370          380          390          400          410          420
sp|Q96 EAARKRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQGWRNVLSAGGSGE
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seqid4 VKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQMQQQRAEDNEAKWKREIYGRGLPER---
      430          440          450          460          470
sp|Q96 VKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQMQQQRAEDNEAKWKREIYGRGLPERGIL
      430          440          450          460          470          480
seqid4 -----
      480          490
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      490          500          510          520          530          540
seqid4 KREAMQNKARAEGHMVYLARLRQIRLQNFNERQQIKAKLRGEKKKEANHSEGGEGSEEADM
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sp|Q96 KREAMQNKARAEGHMVYLARLRQIRLQNFNERQQIKAKLRGEKKKEANHSEGGEGSEEADM
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      670          680          690          700          710          720
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      680          690          700          710          720          730
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      730          740          750          760          770          780
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sp|Q96 TTERHTVGEVIKLGPNGSPRAWGKSPTDSVLKILGEAELQLQT ELLNTTIRSEISPEG
      790          800          810          820          830          840
seqid4 EKYPKLITGEKKVQCISHEINPSAIVDSPVETKSP EFSEASPQMSLKLEG NLEEPDDLET
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sp|Q96 EKYPKLITGEKKVQCISHEINPSAIVDSPVETKSP EFSEASPQMSLKLEG NLEEPDDLET
      850          860          870          880          890          900
seqid4 EILQEPSGTNKDES L PCTITDVWI SEEKETKETQSADR ITTIQENEVS EDGVSSTVDQLSD
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          970           980           990          1000          1010          1020

          980           990          1000          1010          1020          1030
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          1030          1040          1050          1060          1070          1080

          1040          1050          1060          1070          1080          1090
seqid4  EIKDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLR EQPGEEYSEEEEE SVLKNSDV EP
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          1090          1100          1110          1120          1130          1140

          1100          1110          1120          1130          1140          1150
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          1150          1160          1170          1180          1190          1200

          1160          1170          1180          1190          1200          1210
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          1210          1220          1230          1240          1250

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